



PCT

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/509,853

DATE: 10/08/2004  
TIME: 13:50:54

Input Set : A:\sequence listing.txt  
Output Set: N:\CRF4\10082004\J509853.raw

3 <110> APPLICANT: OriGene Technologies, Inc  
5 <120> TITLE OF INVENTION: NOVEL EXPRESSED GENES  
7 <130> FILE REFERENCE: 16U 100 PCT  
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/509,853  
C--> 9 <141> CURRENT FILING DATE: 2004-10-01  
9 <150> PRIOR APPLICATION NUMBER: US 10/112,372  
10 <151> PRIOR FILING DATE: 2002-04-01  
12 <150> PRIOR APPLICATION NUMBER: US 60/382,614  
13 <151> PRIOR FILING DATE: 2002-05-24  
15 <150> PRIOR APPLICATION NUMBER: US 10/164,717  
16 <151> PRIOR FILING DATE: 2002-06-10  
18 <150> PRIOR APPLICATION NUMBER: US 10/167,631  
19 <151> PRIOR FILING DATE: 2002-06-13  
21 <150> PRIOR APPLICATION NUMBER: US 10/177,917  
22 <151> PRIOR FILING DATE: 2002-06-24  
24 <150> PRIOR APPLICATION NUMBER: US 60/399,125  
25 <151> PRIOR FILING DATE: 2002-07-30  
27 <160> NUMBER OF SEQ ID NOS: 59  
29 <170> SOFTWARE: PatentIn version 3.1  
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34 <213> ORGANISM: Homo sapiens  
36 <220> FEATURE:  
37 <221> NAME/KEY: CDS  
38 <222> LOCATION: (242)..(646)  
39 <223> OTHER INFORMATION:

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46 gctaacgaaa gcatgtctga aacaaagcat aactcggtc accggttttc cagtgttgac 180  
48 ctgggggtact gaagcagata gtgtccatat atagatctc accctctgca cttcggggcg 240  
50 c atg gct gac ttc cag ctt cca gat agt att ctc tgg tgc caa aac cta 289  
51 Met Ala Asp Phe Gln Leu Pro Asp Ser Ile Leu Trp Cys Gln Asn Leu  
52 1 5 10 15  
54 ttt tct ctg cct gtt tgg cag tct gga cat act aga gaa ttg atg ctc 337  
55 Phe Ser Leu Pro Val Trp Gln Ser Gly His Thr Arg Glu Leu Met Leu  
56 20 25 30  
58 cag tgt tca gcc ttg agt gat ggg gaa ctg gtg tat aaa tat ccc agc 385  
59 Gln Cys Ser Ala Leu Ser Asp Gly Glu Leu Val Tyr Lys Tyr Pro Ser  
60 35 40 45  
62 tcc ctc act cct tgg ttg agg tta act ctg ggg tgc atg ttc tac act 433  
63 Ser Leu Thr Pro Trp Leu Arg Leu Thr Leu Gly Cys Met Phe Tyr Thr



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64	50	55	60	
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68	65	70	75	80
70	ata gct ggt ttg ata atg cat ctt tta ttg tct ccc tct ctc ctc tgc	529		
71	Ile Ala Gly Leu Ile Met His Leu Leu Leu Ser Pro Ser Leu Leu Cys			
72		85	90	95
74	atc att tcc aca ctc cat tac aga ggt tcc ttg ccc tct caa att att	577		
75	Ile Ile Ser Thr Leu His Tyr Arg Gly Ser Leu Pro Ser Gln Ile Ile			
76		100	105	110
78	agc act cat ttt cca tct cga ctt cta aga atc cag att aga cag gca	625		
79	Ser Thr His Phe Pro Ser Arg Leu Leu Arg Ile Gln Ile Arg Gln Ala			
80		115	120	125
82	tta ttt cat ttg gcc att aag tagatcttgt ggaagctgga ttttcatgcc	676		
83	Leu Phe His Leu Ala Ile Lys			
84	130	135		
86	ataccccgaa agtaggcttt tatgtagaca tcatggaggg tgagggctga gatggaagaa	736		
88	gaggtaaaat tggaccaagg aagagaaccc tgggtgtaagg gttccagctc ttaaaagggg	796		
90	gtcctgggta cctggagggc attattacca gatgacagag gatctggagt ggctcttgct	856		
92	aataagtatc ttgggacaaa gagcagttgc atgcacagag agaaactccc aatgcatgaa	916		
94	gaggagctct tcaaagatga attatgagag gcctattata taaataagga ggcaaaaaga	976		
96	agcaaaggag aaccatcctg ttgtatcaat gtcggagggg ggtgactgtt tgcaccttat	1036		
98	gtgccagaga gagtggctga ctaggaaggc aataccagg gatggaaggg cagaggcaag	1096		
100	accatgggag gccccttttt cagcccatca gatgctcaca actctaattgt ctctcttgca	1156		
102	cttccacggg cagacctctc ccactctgtc ttgggcttcc ctcaattgta tcttctttcc	1216		
104	tcctcttctt gtggagtga tggagagctc tgcagaaggg ggagtctggg gtttaggaga	1276		
106	ccattaaact atctgaatat ctctgatgat gactttgtga aaatgctcct accacctgga	1336		
108	aggataaaca gagcacatca agatttgtaa agacaatacc aagtagagtt cagctgaaaa	1396		
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116	cccctgccct ccatttacta agctctgaat acagatgcag gactgcttca gccagaaaa	1636		
118	aggtgtacta tctcttttct aatctttctg gccagaaagg gcaccttttt ctaattcttg	1696		
120	accataagg agcacctttt tttttcattt aaaaaattta attattatgg ctacataata	1756		
122	gttgtatata ttacagggt atatgtgatg ttccataca ggcatacact atgtaaggat	1816		
124	cagatcaggg taattgtgca tccatctcct caagcatgta tcatttcttt gtgttgga	1876		
126	cattccaaatt acactctttt agttatttta aaatataaga aaaattattg ctaattctcc	1936		
128	cagagtgttg ggattacagg cgtgagccac catgctcggg cttagaagag aataatttga	1996		
130	atgctcccag cataaagaaa ggataaatgt ttaagggtgat ggatatctat ctctattacc	2056		
132	ctgatctgat cattacacat tatgtgaatg tatcgaaata tcacatatat tccaaaaata	2116		
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140	accagctgg atcccacctg ggcctgatca ccagttgtc tctacaataa atgaagtcag	2356		
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146	tggccctgcc ctcagcaagc tccaaacca gtcagagaga tggccaataa aataagcaac	2536		
148	tactgtaccg aggaacaggg ctgtggcaaa caaatgacac tcatttttga atgagtgagt	2596		
150	gaattcaaga ttcagtgaat gaatgaagtg cagtgtattg tgctatcctg gtctggagga	2656		

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156	ggtagaaca	agatgggatg	gcagaaccaa	gaaaactcga	atctgaatca	gtcagcttag	2836
158	gctgtggggg	ccagggtggg	atgggtgtgga	agagatgcta	tttgtgaagt	aggcaggacc	2896
160	ggggtgtaaa	aaacactgtc	atccatgtca	aagagttag	atccattcaa	agaaatggga	2956
162	tttttaaaaa	tgcaggagag	gttgggtattt	tcaggcacca	aatttaaccc	aatgagaaca	3016
164	tttcaatagt	gcctttatcc	ctgttttctg	gtgatgatgg	aaaagcataa	tcctttagtag	3076
166	atttctcagt	tctgaccaca	caagttacat	gtggataagt	cagagccagg	tggtgatact	3136
168	ctgaaagtat	ccctgtgagc	tcagagtgtt	gggttgagaa	gatgaacaag	gctagatcca	3196
170	cttctatatc	cactagccca	gagggggcctc	acattcaaga	aatccttgcc	tacggggatc	3256
172	catggtgcac	caggaaaaat	gaaattcgta	gtcaagacta	ggaacaagta	cttgggagag	3316
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176	cacaggcccc	tgtccttgag	ttcttccagc	ctagctccct	ccaggatggg	cttgttggat	3436
178	tacttgttaa	tacactggct	accaaccact	caccatctct	ggggcaaaga	ttccatgac	3496
180	ccatctttgt	accaagccca	agccagagat	cgcagatctc	agggtctagt	tgcttggcat	3556
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184	aaagatgtgg	catctaaaat	gcaaaaacaag	aagacaaata	aataggagga	ctgaatggga	3676
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222	accccccgcc	atcctgcttc	taaaacgcag	cccgccttcc	caagtgtctg	ctttccatcg	4816
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226	ttattcccag	tcacccccaa	gccccatttc	caagcccctt	ccaaagccct	ctgttgcaag	4936
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238	tcttcccttt	ctcttacacc	ttacctacct	actaaaggag	gagttcttgc	ttggtaagtg	5296
240	gatataatcc	gcaaagacat	gagagaattt	attagaagcc	actcaagagc	cttagctacc	5356
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244	ttggtcagac	tgtttaactt	ccattttttt	tgtccctccc	tttcttttcc	ccttttagttg	5476
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250 <211> LENGTH: 135
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260 Phe Ser Leu Pro Val Trp Gln Ser Gly His Thr Arg Glu Leu Met Leu
261          20          25          30
264 Gln Cys Ser Ala Leu Ser Asp Gly Glu Leu Val Tyr Lys Tyr Pro Ser
265          35          40          45
268 Ser Leu Thr Pro Trp Leu Arg Leu Thr Leu Gly Cys Met Phe Tyr Thr
269          50          55          60
272 Gly Ser Gln Gly Val Leu Thr Glu Ile Lys His Pro Leu Pro Thr Val
273 65          70          75          80
276 Ile Ala Gly Leu Ile Met His Leu Leu Leu Ser Pro Ser Leu Leu Cys
277          85          90          95
280 Ile Ile Ser Thr Leu His Tyr Arg Gly Ser Leu Pro Ser Gln Ile Ile
281          100         105         110
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288 Leu Phe His Leu Ala Ile Lys
289          130         135
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295 <213> ORGANISM: Homo sapiens
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301 <210> SEQ ID NO: 4
302 <211> LENGTH: 25
303 <212> TYPE: DNA
304 <213> ORGANISM: Homo sapiens
306 <400> SEQUENCE: 4
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310 <210> SEQ ID NO: 5
311 <211> LENGTH: 50
312 <212> TYPE: DNA
313 <213> ORGANISM: Homo sapiens
315 <400> SEQUENCE: 5
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319 <210> SEQ ID NO: 6
320 <211> LENGTH: 50
321 <212> TYPE: DNA
322 <213> ORGANISM: Homo sapiens.
324 <400> SEQUENCE: 6
325 aaaaacaata aataacagtg ccggcttccc tggaggggctg agagagactc
328 <210> SEQ ID NO: 7
329 <211> LENGTH: 50
330 <212> TYPE: DNA

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339 <212> TYPE: DNA
340 <213> ORGANISM: Homo sapiens
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347 <211> LENGTH: 50
348 <212> TYPE: DNA
349 <213> ORGANISM: Homo sapiens
351 <400> SEQUENCE: 9
352 ccaagaggga ttaaaaaggt cgagatggga gagatggagc aatacacttc      50
355 <210> SEQ ID NO: 10
356 <211> LENGTH: 50
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358 <213> ORGANISM: Homo sapiens
360 <400> SEQUENCE: 10
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364 <210> SEQ ID NO: 11
365 <211> LENGTH: 2270
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367 <213> ORGANISM: Homo sapiens
369 <220> FEATURE:
370 <221> NAME/KEY: CDS
371 <222> LOCATION: (157)..(1080)
372 <223> OTHER INFORMATION:
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379 tgggggactg tgtgagctgg aaacgtggct ggccag atg ggc agc acc atg gag      174
380                                     Met Gly Ser Thr Met Glu
381                                     1               5
383 ccc cct ggg ggt gcg tac ctg cac ctg ggc gcc gtg aca tcc cct gtg      222
384 Pro Pro Gly Gly Ala Tyr Leu His Leu Gly Ala Val Thr Ser Pro Val
385          10               15               20
387 ggc aca gcc cgc gtg ctg cag ctg gcc ttt ggc tgc act acc ttc agc      270
388 Gly Thr Ala Arg Val Leu Gln Leu Ala Phe Gly Cys Thr Thr Phe Ser
389          25               30               35
391 ctg gtg gct cac cgg ggt ggc ttt gcg ggc gtc cag ggc acc ttc tgc      318
392 Leu Val Ala His Arg Gly Gly Phe Ala Gly Val Gln Gly Thr Phe Cys
393          40               45               50
395 atg gcc gcc tgg ggc ttc tgc ttc gcc gtc tct gcg ctg gtg gtg gcc      366
396 Met Ala Ala Trp Gly Phe Cys Phe Ala Val Ser Ala Leu Val Val Ala
397 55          60          65          70
399 tgt gag ttc aca cgg ctc cac ggc tgc ctg cgg ctc tcc tgg ggc aac      414
400 Cys Glu Phe Thr Arg Leu His Gly Cys Leu Arg Leu Ser Trp Gly Asn

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## VERIFICATION SUMMARY

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L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
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